FIGURE 1

TTCGCCCTTCTGTGCTCTGCCTCTGAGGAGACC**ATG**GCCCAGTATCTGAGTACCCTGCTGCTCCTGCTGGCCAC

CCTAGCTGTGGCCCTGGCCTGGAGCCCCAAGGAGGAGGATAGGATAATCCCGGGTGGCATCTATAACGCAGACC

TCAATGATGAGTGGGTACAGCGTGCCCTTCACTTCGCCATCAGCGAGTATAACAAGGCCACCAAAGATGACTAC

TACAGACGTCCGCTGCGGGTACTAAGAGCCAGGCAACAGACCGTTGGGGGGGTGAATTACTTCTTCGACGTAGA

GGTGGGCCGAACCATATGTACCAAGTCCCAGCCCAACTTGGACACCTGTGCCTTCCATGAACAGCCAGAACTGC

AGAAGAAACAGTTGTGCTCTTTCGAGATCTACGAAGTTCCCTGGGAGAACAGAAGGTCCCTGGTGAATTCCAGG

TGTCAAGAAGCC**TAG**GGAAGGGCGA

FIGURE 2

GCCTCCGAGGAGACC**ATG**GCCTGGCCCCTGTGCACCCTGCTGCTCCTGCTGGCCACCCAGGCTGTGGCCCTGGC

CTGGAGCCCCCAGGAGGAGGACAGGATAATCGAGGGTGGCATCTATGATGCAGACCTCAATGATGAGCGGGTAC

AGCGTGCCCTTCACTTTGTCATCAGCGAGTATAACAAGGCCACTGAAGATGAGTACTACAGACGCCTGCTGCGG

GTGCTACGAGCCAGGGAGCAGATCGTGGGCGGGGTGAATTACTTCTTCGACATAGAGGTGGGCCGAACCATATG

TACCAAGTCCCAGCCCAACTTGGACACCTGTGCCTTCCATGAACAGCCAGAACTGCAGAAGAAACAGTTGTGCT

CTTTCCAGATCTACGAAGTTCCCTGGGAGGACAGAATGTCCCTGGTGAATTCCAGGTGTCAAGAAGCC**TAG**GGA

TCTGTGCCAGGGAGTCACACTGACCACCTCCTACTCCCACCCCTTGTAGTGCTCCCACCCCTGGACTGGTGGCC

CCCACCCTGTGGGAGGTCTCCCCATGCACCTGCAGCAGGAGAAGACAGAGAAGGCTGCAGGAGGCCTTTGTTGC

TCAGCAGGGGACTCTGCCCTCCCTCCTTCCTTTTGCTTCTCATAGCCCTGGTACATGGTACACACACCCCCACC

TCCTGCAATTAAACAGTAGCATCACCTC

FIGURE 3

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**ATG**GCTTCCCTGGG

GCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTG

GTATTTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTG

AGCTGCACTTTTGAACCTGACATCAAACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTT

GGTCCATGAGTTCAAAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTCAGAGGCCGGACAGCAGTGT

TTGCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTAC

AAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCC

GGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCA

CAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAAC

TCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGAT

TGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAGTCACCTAC

AGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGC

CCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTAC

AGAACTATTTCACCACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGG

AGTGAGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATC

TTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAAT

GCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGGAGTGAGAGGACAGG

ATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCTGGAAAG

TCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGA

CTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAA

AGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAG

AGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAAAAA

AAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 4

MAQYLSTLLLLLATLAVALAWSPKEEDRIIPGGIYNADLNDEWVQRALHFAISEYNKATKDDYYRRPLRVLRAR
QQTVGGVNYFFDVEVGRTICTKSQPNLDTCAFHEQPELQKKQLCSFEIYEVPWENRRSLVNSRCQEA

Signal sequence.
amino acids 1-20

Tyrosine kinase phosphorylation site.
amino acids 57-64

N-myristoylation sites.
amino acids 32-37, 33-38

Myb DNA-binding domain repeat signature 1.
amino acids 21-29

Cystatin domain.
amino acids 32-137

FIGURE 5

MAWPLCTLLLLLATQAVALAWSPQEEDRIIEGGIYDADLNDERVQRALHFVISEYNKATEDEYYRRLLRVLRAR
EQIVGGVNYFFDIEVGRTICTKSQPNLDTCAFHEQPELQKKQLCSFQIYEVPWEDRMSLVNSRCQEA

Signal sequence.
amino acids 1-20

Tyrosine kinase phosphorylation sites.
amino acids 28-35, 57-64

N-myristoylation site.
amino acids 33-38

Myb DNA-binding domain repeat signature 1.
amino acids 21-29

Cystatin domain.
amino acids 32-137

FIGURE 6

MASLGQILFWSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKE
GVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTG
AFSMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNT
YSCMIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

Signal peptide.
amino acids 1-28

Transmembrane domain.
amino acids 258-281

N-glycosylation sites.
amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

N-myristoylation sites.
amino acids 52-58, 126-132, 188-194

Immunoglobulin domain.
amino acids 49-132